

SEQUENCE LISTING

<110> Acton, Susan

<120> NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR

<130> MNI-050

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<170> PatentIn Ver. 2.0

<210> 1

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<212> DNA

<213> Homo sapiens

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<223> 'n' at positions 2872, 3597 and 3682 may be any nucleic acid

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<222> (297)..(1202)

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Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu			
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35

40

45

Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
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Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
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Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
 85 90 95

Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
 100 105 110

Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
 115 120 125

Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
 130 135 140

Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
 145 150 155 160

Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
 165 170 175

Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
 180 185 190

Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
 195 200 205

His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
 210 215 220

Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
 225 230 235 240

Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
 245 250 255

Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
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 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
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aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt 144
 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
 35 40 45

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 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
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gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc 240
 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
 65 70 75 80

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 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
 85 90 95

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 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
 100 105 110

cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag 384
 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
 115 120 125

caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag 432
 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
 130 135 140

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 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
 145 150 155 160

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gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata 624
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 195 200 205

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 210 215 220

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 225 230 235 240

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 245 250 255

cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat 816
 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
 260 265 270

atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt 864
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gaa aac tgc ggt gga gga agt ttt ggg agt gtt tat cga gcc aaa tgg 151
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ata tca cag gac aag gag gtg gct gta aag aag ctc ctc aaa ata gag 199
 Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu Lys Ile Glu
 40 45 50

aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac atc atc cag 247
 Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn Ile Ile Gln
 55 60 65

ttt tat gga gta att ctt gaa cct ccc aac tat ggc att gtc aca gaa 295
 Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile Val Thr Glu
 70 75 80

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gag gag atg gat atg gat cac att atg acc tgg gcc act gat gta gcc Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr Asp Val Ala	100	105	110	115	391	
aaa gga atg cat tat tta cat atg gag gct cct gtc aag gtg att cac Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys Val Ile His	120	125	130		439	
aga gac ctc aag tca aga aac gtt gtt ata gct gct gat gga gta ctg Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp Gly Val Leu	135	140	145		487	
aag atc tgt gac ttt ggt gcc tct cgg ttc cat aac cat aca aca cac Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His Thr Thr His	150	155	160		535	
atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa gtt atc cag Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu Val Ile Gln	165	170	175		583	
agt ctc cct gtg tca gaa act tgt gac aca tat tcc tat ggt gtg gtt Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr Gly Val Val	180	185	190	195		631
ctc tgg gag atg cta aca agg gag gtc ccc ttt aaa ggt ttg gaa gga Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly Leu Glu Gly	200	205	210			679
tta caa gta gct tgg ctt gta gtg gaa aaa aac gag aga tta acc att Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg Leu Thr Ile	215	220	225			727
cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat cag tgt tgg Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His Gln Cys Trp	230	235	240			775
gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc att tca atc Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile Ile Ser Ile	245	250	255			823
ctg gag tcc atg tca aat gac acg agc ctt cct gac aag tgt aac tca Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys Cys Asn Ser	260	265	270	275		871
ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag gca act ctt Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu Ala Thr Leu	280	285	290			919
gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag gag cag gag Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys Glu Gln Glu	295	300	305			967

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Glu Gln Ser Asn Thr Pro Leu Leu Pro Leu Ala Ala Arg Met Ser				
gag gag tct tac ttt gaa tct aaa aca gag gag tca aac agt gca gag	340	345	350	1111
Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn Ser Ala Glu				
atg tca tgt cag atc aca gca aca agt aac ggg gag ggc cat ggc atg	360	365	370	1159
Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly His Gly Met				
aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg gat atc ttc	375	380	385	1207
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tca atg aac aaa gca gga gct gtg atg cat tct ggg atg cag ata aac	390	395	400	1255
Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met Gln Ile Asn				
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Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys Arg Arg Gly				
aag aaa gtc aac atg gct ctg ggg ttc agt gat ttt gac ttg tca gaa	420	425	430	1351
Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp Leu Ser Glu				
ggt gac gat gat gat gac ggt gag gag qag gat aat gac atg	440	445	450	1399
Gly Asp Asp Asp Asp Asp Asp Gly Glu Glu Asp Asn Asp Met				
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 Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn
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 Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile
 65 70 75 80
 Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser
 85 90 95
 Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr
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 Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys
 115 120 125
 Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp
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 Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His
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 Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu
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 Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr
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 Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly
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 Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His

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225	230	235	240
Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile			
245	250	255	
Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys			
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Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu			
275	280	285	
Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys			
290	295	300	
Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln			
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Lys Leu Thr Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala			
325	330	335	
Arg Met Ser Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn			
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His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly			
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Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met			
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Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys			
405	410	415	
Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp			
420	425	430	
Leu Ser Glu Gly Asp Asp Asp Asp Asp Asp Gly Glu Glu Asp			
435	440	445	
Asn Asp Met Asp Asn Ser Glu			
450	455		

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)...(1365)

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 Met Ser Ser Leu Gly Ala Ser Phe Val Gln Ile Lys Phe Asp Asp Leu

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5

10

15

cag ttt ttt gaa aac tgc ggt gga gga agt ttt ggg agt gtt tat cga Gln Phe Phe Glu Asn Cys Gly Gly Ser Phe Gly Ser Val Tyr Arg 20 25 30	96
gcc aaa tgg ata tca cag gac aag gag gtg gct gta aag aag ctc ctc Ala Lys Trp Ile Ser Gln Asp Lys Glu Val Ala Val Lys Lys Leu Leu 35 40 45	144
aaa ata gag aaa gag gca gaa ata ctc agt gtc ctc agt cac aga aac Lys Ile Glu Lys Glu Ala Glu Ile Leu Ser Val Leu Ser His Arg Asn 50 55 60	192
atc atc cag ttt tat gga gta att ctt gaa cct ccc aac tat ggc att Ile Ile Gln Phe Tyr Gly Val Ile Leu Glu Pro Pro Asn Tyr Gly Ile 65 70 75 80	240
gtc aca gaa tat gct tct ctg gga tca ctc tat gat tac att aac agt Val Thr Glu Tyr Ala Ser Leu Gly Ser Leu Tyr Asp Tyr Ile Asn Ser 85 90 95	288
aac aga agt gag gag atg gat atg gat cac att atg acc tgg gcc act Asn Arg Ser Glu Glu Met Asp Met Asp His Ile Met Thr Trp Ala Thr 100 105 110	336
gat gta gcc aaa gga atg cat tat tta cat atg gag gct cct gtc aag Asp Val Ala Lys Gly Met His Tyr Leu His Met Glu Ala Pro Val Lys 115 120 125	384
gtg att cac aga gac ctc aag tca aga aac gtt gtt ata gct gct gat Val Ile His Arg Asp Leu Lys Ser Arg Asn Val Val Ile Ala Ala Asp 130 135 140	432
gga gta ctg aag atc tgt gac ttt ggt gcc tct cgg ttc cat aac cat Gly Val Leu Lys Ile Cys Asp Phe Gly Ala Ser Arg Phe His Asn His 145 150 155 160	480
aca aca cac atg tcc ttg gtt gga act ttc cca tgg atg gct cca gaa Thr Thr His Met Ser Leu Val Gly Thr Phe Pro Trp Met Ala Pro Glu 165 170 175	528
gtt atc cag agt ctc cct gtg tca gaa act tgt gac aca tat tcc tat Val Ile Gln Ser Leu Pro Val Ser Glu Thr Cys Asp Thr Tyr Ser Tyr 180 185 190	576
ggt gtg gtt ctc tgg gag atg cta aca agg gag gtc ccc ttt aaa ggt Gly Val Val Leu Trp Glu Met Leu Thr Arg Glu Val Pro Phe Lys Gly 195 200 205	624
ttg gaa gga tta caa gta gct tgg ctt gta gtg gaa aaa aac gag aga Leu Glu Gly Leu Gln Val Ala Trp Leu Val Val Glu Lys Asn Glu Arg 210 215 220	672
tta acc att cca agc agt tgc ccc aga agt ttt gct gaa ctg tta cat Leu Thr Ile Pro Ser Ser Cys Pro Arg Ser Phe Ala Glu Leu Leu His 225 230 235 240	720

cag tgt tgg gaa gct gat gcc aag aaa cgg cca tca ttc aag caa atc Gln Cys Trp Glu Ala Asp Ala Lys Lys Arg Pro Ser Phe Lys Gln Ile 245 250 255	768
att tca atc ctg gag tcc atg tca aat gac acg agc ctt cct gac aag Ile Ser Ile Leu Glu Ser Met Ser Asn Asp Thr Ser Leu Pro Asp Lys 260 265 270	816
tgt aac tca ttc cta cac aac aag gcg gag tgg agg tgc gaa att gag Cys Asn Ser Phe Leu His Asn Lys Ala Glu Trp Arg Cys Glu Ile Glu 275 280 285	864
gca act ctt gag agg cta aag aaa cta gag cgt gat ctc agc ttt aag Ala Thr Leu Glu Arg Leu Lys Lys Leu Glu Arg Asp Leu Ser Phe Lys 290 295 300	912
gag cag gag ctt aaa gaa cga gaa aga cgt tta aag atg tgg gag caa Glu Gln Glu Leu Lys Glu Arg Glu Arg Arg Leu Lys Met Trp Glu Gln 305 310 315 320	960
aag ctg aca gag cag tcc aac acc ccg ctt ctc ttg cct ctt gct gca Lys Leu Thr Glu Gln Ser Asn Thr Pro Leu Leu Leu Pro Leu Ala Ala 325 330 335	1008
aga atg tct gag gag tct tac ttt gaa tct aaa aca gag gag tca aac Arg Met Ser Glu Glu Ser Tyr Phe Glu Ser Lys Thr Glu Glu Ser Asn 340 345 350	1056
agt gca gag atg tca tgt cag atc aca gca aca agt aac ggg gag ggc Ser Ala Glu Met Ser Cys Gln Ile Thr Ala Thr Ser Asn Gly Glu Gly 355 360 365	1104
cat ggc atg aac cca agt ctg cag gcc atg atg ctg atg ggc ttt ggg His Gly Met Asn Pro Ser Leu Gln Ala Met Met Leu Met Gly Phe Gly 370 375 380	1152
gat atc ttc tca atg aac aaa gca gga gct gtg atg cat tct ggg atg Asp Ile Phe Ser Met Asn Lys Ala Gly Ala Val Met His Ser Gly Met 385 390 395 400	1200
cag ata aac atg caa gcc aag cag aat tct tcc aaa acc aca tct aag Gln Ile Asn Met Gln Ala Lys Gln Asn Ser Ser Lys Thr Thr Ser Lys 405 410 415	1248
aga agg ggg aag aaa gtc aac atg gct ctg ggg ttc agt gat ttt gac Arg Arg Gly Lys Lys Val Asn Met Ala Leu Gly Phe Ser Asp Phe Asp 420 425 430	1296
ttg tca gaa ggt gac gat gat gat gat gac ggt gag gag gag gat Leu Ser Glu Gly Asp Asp Asp Asp Asp Asp Gly Glu Glu Glu Asp 435 440 445	1344
aat gac atg gat aat agt gaa Asn Asp Met Asp Asn Ser Glu 450 455	1365

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<220>
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<400> 7

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					1		
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Val Arg Gln	Ala Leu Gly	Arg Gly Leu	Gln Leu Gly	Arg Ala	Leu Leu		
5	10		15				
ctg cgc ttc acg	ggc aag	ccc ggc	cggttac	ggc ttg	ggg cgg	ccg	152
Leu Arg Phe	Thr Gly Lys	Pro Gly Arg	Ala Tyr Gly	Leu Gly Arg	Arg Pro		
20	25		30				
ggc ccg gcg	gctgt	gtc cgc	ggggag	cgt cca	ggc tgg	gcc gca	200
Gly Pro Ala	Ala Gly Val	Arg Gly Glu	Arg Pro Gly	Trp Ala	Ala		
35	40		45		50		
gga ccg ggc	gctcagg	gtcggg	ctctt	cctaac	cgtt	ccgtt	248
Gly Pro Ala	Glu Pro Arg	Arg Val Gly	Leu Gly Leu	Pro Asn	Arg		
55	60		65				
ctc cgc ttc	tcgcag	tcgtcg	gggctc	gggtt	cttcc	tttcc	296
Leu Arg Phe	Phe Arg Gln	Ser Val Ala	Gly Leu Ala	Ala Arg	Leu Gln		
70	75		80				
cgg cag ttc	gtggcc	tggggc	tgcgcg	ccttgc	ggccgt	ccgg	344
Arg Gln Phe	Val Val Arg	Ala Trp Gly	Cys Ala Gly	Pro Cys	Gly Arg		
85	90		95				
gca gtc ttt	ctggcc	tttggg	ctgtgg	cttcatc	gagaaa	aaa	392
Ala Val Phe	Leu Ala Phe	Gly Leu Gly	Leu Gly Leu	Ile Glu	Glu Lys		
100	105		110				
cag gcg gag	agc cgg	cggtcg	tgtcag	gagatc	cagcag	gca	440
Gln Ala Glu	Ser Arg Arg	Ala Val Ser	Ala Cys	Gln Glu	Ile Gln	Ala	
115	120		125		130		
att ttt acc	cag aaa	agc aag	ccggcc	cctgac	ccgttgc	acg aga	488
Ile Phe Thr	Gln Lys Ser	Lys Pro	Gly Pro	Asp Pro	Leu Asp	Thr Arg	
135	140		145				
cgc ttg cag	ggcttt	cggttg	gagtat	ctgata	gggcag	tccatt	536
Arg Leu Gln	Gly Phe Arg	Leu Glu	Tyr Leu Ile	Gly Gln	Ser Ile		
150	155		160				
ggt aag ggc	tgc agt	gct gtc	gttat	gaa gcc	acc atg	cct aca	584
Gly Lys Gly	Cys Ser Ala	Ala Val	Tyr Glu Ala	Thr Met	Pro Thr	Leu	

165	170	175	
ccc cag aac ctg gag gtg aca aag agc acc ggg ttg ctt cca ggg aga Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro Gly Arg 180	185	190	
ggc cca ggt acc agt gca cca gga gaa ggg cag gag cga gct ccg ggg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala Pro Gly 195	200	205	680
gcc cct gcc ttc ccc ttg gcc atc aag atg atg tgg aac atc tcg gca Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile Ser Ala 215	220	225	728
ggt tcc tcc agc gaa gcc atc ttg aac aca atg agc cag gag ctg gtc Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu Leu Val 230	235	240	776
cca gcg agc cga gtg gcc ttg gct ggg gag tat gga gca gtc act tac Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val Thr Tyr 245	250	255	824
aga aaa tcc aag aga ggt ccc aag caa cta gcc cct cac ccc aac atc Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro Asn Ile 260	265	270	872
atc cgg gtt ctc cgc gcc ttc acc tct tcc gtg ccg ctg ctg cca ggg Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu Pro Gly 275	280	285	920
gcc ctg gtc gac tac cct gat gtg ctg ccc tca cgc ctc cac cct gaa Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His Pro Glu 295	300	305	968
ggc ctg ggc cat ggc cgg acg ctg ttc ctc gtt atg aag aac tat ccc Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn Tyr Pro 310	315	320	1016
tgt acc ctg cgc cag tac ctt tgt gtg aac aca ccc agc ccc cgc ctc Cys Thr Leu Arg Cln Tyr Leu Cys Val Asn Thr Pro Ser Pro Arg Leu 325	330	335	1064
gcc gcc atg atg ctg ctg cag ctg ctg gaa ggc gtg gac cat ctg gtt Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His Leu Val 340	345	350	1112
caa cag ggc atc gcg cac aga gac ctg aaa tcc gac aac atc ctt gtg Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile Leu Val 355	360	365	1160
gag ctg gac cca gac ggc tgc ccc tgg ctg gtg atc gca gat ttt ggc Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp Phe Gly 375	380	385	1208
tgc tgc ctg gct gat gag agc atc ggc ctg cag ttg ccc ttc agc agc Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe Ser Ser 390	395	400	1256

tgg tac gtg gat cgg ggc aac ggc tgt ctg atg gcc cca gag gtg Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro Glu Val 405 410 415	1304
tcc acg gcc cgt cct ggc ccc agg gca gtg att gac tac agc aag gct Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser Lys Ala 420 425 430	1352
gat gcc tgg gca gtg gga gcc atc gcc tat gaa atc ttc ggg ctt gtc Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly Leu Val 435 440 445 450	1400
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caa gag gct cag cta cct gca ctg ccc gag tca gtg cct cca gac gtg Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro Asp Val 470 475 480	1496
aga cag ttg gtg agg gca ctg ctc cag cga gag gcc agc aag aga cca Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys Arg Pro 485 490 495	1544
tct gcc cga gta gcc gca aat gtg ctt cat cta agc ctc tgg ggt gaa Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp Gly Glu 500 505 510	1592
cat att cta gcc ctg aag aat ctg aag tta gac aag atg gtt ggc tgg His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val Gly Trp 515 520 525 530	1640
ctc ctc caa caa tcg gcc gcc act ttg ttg gcc aac agg ctc aca gag Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu Thr Glu 535 540 545	1688
aag tgt tgt gtg gaa aca aaa atg aag atg ctc ttt ctg gct aac ctg Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala Asn Leu 550 555 560	1736
gag tgt gaa acg ctc tgc cag gca gcc ctc ctc tgc tca tgg agg Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser Trp Arg 565 570 575	1784
gca gcc ctg tcatgtccct gcatggagct ggtgaattac taaaagaact Ala Ala Leu 580	1833
tggcatcctc tgtgtcgtga tggctgtga atggtgaggg tgggagtcag gagacaagac 1893	
agcgcagaga gggctggta gccggaaaag gcctcggtt tggcaatgg aagaacttga 1953	
gtgagagttc agtctgcagt cctctgctca cagacatctg aaaagtgaat ggccaagctg 2013	
gtcttagtaga tgaggctgga ctgaggaggg ttaggcctgc atccacagag aggatccagg 2073	

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 cggatgagca gtaagtaagt aagtgtgggg atttaaactt gagggtttcc ctcctgacta 2373
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 35 40 45
 Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro
 50 55 60
 Asn Arg Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg
 65 70 75 80
 Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys
 85 90 95
 Cly Arg Ala Val Phe Leu Ala Phe Cly Leu Cly Leu Cly Leu Ile Clu
 100 105 110
 Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile
 115 120 125
 Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp
 130 135 140
 Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln
 145 150 155 160
 Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro
 165 170 175
 Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro
 180 185 190

Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala
195 200 205

Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile
210 215 220

Ser Ala Gly Ser Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu
225 230 235 240

Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val
245 250 255

Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro
260 265 270

Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu
275 280 285

Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His
290 295 300

Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn
305 310 315 320

Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro
325 330 335

Arg Leu Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His
340 345 350

Leu Val Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile
355 360 365

Leu Val Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp
370 375 380

Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe
385 390 395 400

Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro
405 410 415

Glu Val Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser
420 425 430

Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly
435 440 445

Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg
450 455 460

Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro
465 470 475 480

Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys
485 490 495

Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp
 500 505 510

Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val
 515 520 525

Gly Trp Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu
 530 535 540

Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala
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Asn Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Leu Cys Ser
 565 570 575

Trp Arg Ala Ala Leu
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ctg ctg ctg cgc ttc acg ggc aag ccc qgc cgg gcc tac ggc ttg qgg 96
 Leu Leu Leu Arg Phe Thr Gly Lys Pro Gly Arg Ala Tyr Gly Leu Gly
 20 25 30

cgg ccg ggc ccg gcg ggc tgc cgc ggg gag cgt cca ggc tgg 144
 Arg Pro Gly Pro Ala Ala Gly Cys Val Arg Gly Glu Arg Pro Gly Trp
 35 40 45

gcc gca gga ccg ggc gcg gag cct cgc agg gtc ggg ctc ggg ctt cct 192
 Ala Ala Gly Pro Gly Ala Glu Pro Arg Arg Val Gly Leu Gly Leu Pro
 50 55 60

aac cgt ctc cgc ttc cgc cag tcg gtg gcc ggg ctg gcg gcg 240
 Asn Arg Leu Arg Phe Phe Arg Gln Ser Val Ala Gly Leu Ala Ala Arg
 65 70 75 80

ttg cag cgg cag ttc gtg gtg cgg gcc tgg ggc tgc gcg ggc cct tgc 288
 Leu Gln Arg Gln Phe Val Val Arg Ala Trp Gly Cys Ala Gly Pro Cys
 85 90 95

ggc cgg gca gtc ttt ctg gcc ttc ggg cta ggg ctg ggc ctc atc gag 336
 Gly Arg Ala Val Phe Leu Ala Phe Gly Leu Gly Leu Gly Leu Ile Glu
 100 105 110

gaa aaa cag gcg gag agc cgg cgg gtc tcg gcc tgt cag gag atc	384
Glu Lys Gln Ala Glu Ser Arg Arg Ala Val Ser Ala Cys Gln Glu Ile	
115 120 125	
cag gca att ttt acc cag aaa agc aag ccg ggg cct gac ccg ttg gac	432
Gln Ala Ile Phe Thr Gln Lys Ser Lys Pro Gly Pro Asp Pro Leu Asp	
130 135 140	
acg aga cgc ttg cag ggc ttt cgg ctg gag gag tat ctg ata ggg cag	480
Thr Arg Arg Leu Gln Gly Phe Arg Leu Glu Glu Tyr Leu Ile Gly Gln	
145 150 155 160	
tcc att ggt aag ggc tgc agt gct gtc tat gaa gcc acc atg cct	528
Ser Ile Gly Lys Gly Cys Ser Ala Ala Val Tyr Glu Ala Thr Met Pro	
165 170 175	
aca ttg ccc cag aac ctg gag gtg aca aag agc acc ggg ttg ctt cca	576
Thr Leu Pro Gln Asn Leu Glu Val Thr Lys Ser Thr Gly Leu Leu Pro	
180 185 190	
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Gly Arg Gly Pro Gly Thr Ser Ala Pro Gly Glu Gly Gln Glu Arg Ala	
195 200 205	
ccg ggg gcc cct gcc ttc ccc ttg gcc atc aag atg atg tgg aac atc	672
Pro Gly Ala Pro Ala Phe Pro Leu Ala Ile Lys Met Met Trp Asn Ile	
210 215 220	
tcg gca ggt tcc tcc agc gaa gcc atc ttg aac aca atg agc cag gag	720
Ser Ala Gly Ser Ser Glu Ala Ile Leu Asn Thr Met Ser Gln Glu	
225 230 235 240	
ctg gtc cca gcg agc cga gtg gcc ttg gct ggg gag tat gga gca gtc	768
Leu Val Pro Ala Ser Arg Val Ala Leu Ala Gly Glu Tyr Gly Ala Val	
245 250 255	
act tac aga aaa tcc aag aga ggt ccc aag caa cta gcc cct cac ccc	816
Thr Tyr Arg Lys Ser Lys Arg Gly Pro Lys Gln Leu Ala Pro His Pro	
260 265 270	
aac atc atc cgg gtt ctc cgc gcc ttc acc tct tcc gtg ccg ctg ctg	864
Asn Ile Ile Arg Val Leu Arg Ala Phe Thr Ser Ser Val Pro Leu Leu	
275 280 285	
cca ggg gcc ctg gtc gac tac cct gat gtg ctg ccc tca cgc ctc cac	912
Pro Gly Ala Leu Val Asp Tyr Pro Asp Val Leu Pro Ser Arg Leu His	
290 295 300	
cct gaa ggc ctg ggc cat ggc cgg acg ctg ttc ctc gtt atg aag aac	960
Pro Glu Gly Leu Gly His Gly Arg Thr Leu Phe Leu Val Met Lys Asn	
305 310 315 320	
tat ccc tgt acc ctg cgc cag tac ctt tgt gtg aac aca ccc agc ccc	1008
Tyr Pro Cys Thr Leu Arg Gln Tyr Leu Cys Val Asn Thr Pro Ser Pro	
325 330 335	
cgc ctc gcc gcc atg atg ctg ctg cag ctg ctg gaa ggc gtg gac cat	1056

100

Arg Leu Ala Ala Met Met Leu Leu Gln Leu Leu Glu Gly Val Asp His			
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Leu Val Gln Gln Gly Ile Ala His Arg Asp Leu Lys Ser Asp Asn Ile			
355	360	365	
ctt gtg gag ctg gac cca gac ggc tgc ccc tgg ctg gtg atc gca gat		1152	
Leu Val Glu Leu Asp Pro Asp Gly Cys Pro Trp Leu Val Ile Ala Asp			
370	375	380	
ttt ggc tgc tgc ctg gct gat gag agc atc ggc ctg cag ttg ccc ttc		1200	
Phe Gly Cys Cys Leu Ala Asp Glu Ser Ile Gly Leu Gln Leu Pro Phe			
385	390	395	400
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Ser Ser Trp Tyr Val Asp Arg Gly Gly Asn Gly Cys Leu Met Ala Pro			
405	410	415	
gag gtg tcc acg gcc cgt cct ggc ccc agg gca gtg att gac tac agc		1296	
Glu Val Ser Thr Ala Arg Pro Gly Pro Arg Ala Val Ile Asp Tyr Ser			
420	425	430	
aag gct gat gcc tgg gca gtg gga gcc atc gcc tat gaa atc ttc ggg		1344	
Lys Ala Asp Ala Trp Ala Val Gly Ala Ile Ala Tyr Glu Ile Phe Gly			
435	440	445	
ctt gtc aat ccc ttc tac ggc cag ggc aag gcc cac ctt gaa agc cgc		1392	
Leu Val Asn Pro Phe Tyr Gly Gln Gly Lys Ala His Leu Glu Ser Arg			
450	455	460	
agc tac caa gag gct cag cta cct gca ctg ccc gag tca gtg cct cca		1440	
Ser Tyr Gln Glu Ala Gln Leu Pro Ala Leu Pro Glu Ser Val Pro Pro			
465	470	475	480
gac gtg aga cag ttg gtg agg gca ctg ctc cag cga gag gcc agc aag		1488	
Asp Val Arg Gln Leu Val Arg Ala Leu Leu Gln Arg Glu Ala Ser Lys			
485	490	495	
aga cca tct gcc cga gta gcc gca aat gtg ctt cat cta agc ctc tgg		1536	
Arg Pro Ser Ala Arg Val Ala Ala Asn Val Leu His Leu Ser Leu Trp			
500	505	510	
ggg gaa cat att cta gcc ctg aag aat ctg aag tta gac aag atg gtt		1584	
Gly Glu His Ile Leu Ala Leu Lys Asn Leu Lys Leu Asp Lys Met Val			
515	520	525	
ggc tgg ctc ctc caa caa tcg gcc gcc act ttg ttg gcc aac agg ctc		1632	
Gly Trp Leu Leu Gln Gln Ser Ala Ala Thr Leu Leu Ala Asn Arg Leu			
530	535	540	
aca gag aag tgt tgt gtg gaa aca aaa atg aag atg ctc ttt ctg gct		1680	
Thr Glu Lys Cys Cys Val Glu Thr Lys Met Lys Met Leu Phe Leu Ala			
545	550	555	560
aac ctg gag tgt gaa acg ctc tgc cag gca gcc ctc ctc tgc tca		1728	
Asn Leu Glu Cys Glu Thr Leu Cys Gln Ala Ala Leu Leu Cys Ser			

101

565

570

575

tgg agg gca gcc ctg	1743
Trp Arg Ala Ala Leu	
580	
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cgctttgag tccgttgaag acacaatttc tctctgtcgg gtgcttagga ggagctccat 120	
gaacatgtat tgaattggac ttagctgaac aggctgctgg ttggctgccc agagggggca 180	
ggctgtgttgc tgggagcct tccagctccc tgcagcagtc atggggcagg gttccccgag 240	
tccgtaatcc ccatttccac ctactttccc ttag tta ttt gat tcc ctg tct gtc 295	
Leu Phe Asp Ser Leu Ser Val	
1 5	
gta ctc agc tta agt gga gca tcc cct ttc ctg gga gac acg aag cag 343	
Val Leu Ser Leu Ser Gly Ala Ser Pro Phe Leu Gly Asp Thr Lys Gln	
10 15 20	
gaa aca ctg gca aat atc aca gca gtg agt tac gac ttt gat gag gaa 391	
Glu Thr Leu Ala Asn Ile Thr Ala Val Ser Tyr Asp Phe Asp Glu Glu	
25 30 35	
ttc ttc agc cag acg agc gag ctg gcc aag gac ttt att cgg aag ctt 439	
Phe Phe Ser Gln Thr Ser Glu Leu Ala Lys Asp Phe Ile Arg Lys Leu	
40 45 50 55	
ctg gtt aaa gag acc cgg aaa cgg ctc aca atc caa gag gct ctc aga 487	
Leu Val Lys Glu Thr Arg Lys Arg Leu Thr Ile Gln Glu Ala Leu Arg	
60 65 70	
cac ccc tgg atc acg ccg gtg gac aac cag caa gcc atg gtg cgc agg 535	
His Pro Trp Ile Thr Pro Val Asp Asn Gln Gln Ala Met Val Arg Arg	
75 80 85	
gag tct gtg gtc aat ctg gag aac ttc agg aag cag tat gtc cgc agg 583	
Glu Ser Val Val Asn Leu Glu Asn Phe Arg Lys Gln Tyr Val Arg Arg	
90 95 100	
cggtgg aag ctt tcc ttc agc atc gtg tcc ctg tgc aac cac ctc acc 631	
Arg Trp Lys Leu Ser Phe Ser Ile Val Ser Leu Cys Asn His Leu Thr	
105 110 115	

cgc tcg ctg atg aag aag gtg cac ctg agg ccg gat gag gac ctg agg 679
 Arg Ser Leu Met Lys Lys Val His Leu Arg Pro Asp Glu Asp Leu Arg
 120 125 130 135

 aac tgt gag agt gac act gag gag gac atc gcc agg agg aaa gcc ctc 727
 Asn Cys Glu Ser Asp Thr Glu Glu Asp Ile Ala Arg Arg Lys Ala Leu
 140 145 150

 cac cca cgg agg agg agc agc acc tcc taactggcct gaccgtcagt 774
 His Pro Arg Arg Ser Ser Thr Ser
 155 160

 ggccgccagg gaggtctggg cccagcgggg ctcccttctg tgcagacttt tggacccagc 834
 tcageaccag caccggggcg tcctgagcac tttgcaagag agatggggcc aaggaattca 894
 gaagagctt caggcaagcc aggagaccct gggagctgtg gctgtttct gtggaggagg 954
 ctccagcatt cccaaagctc ttaattctcc ataaaatggg ctttcctctg tctgccatcc 1014
 tcagagtctg gggtgggagt gtggacttag gaaaacaata taaaggacat cctcatcatc 1074
 acggggtgaa ggtcagacta aggccgcctt cttcacaggc tgagggggtt cagaaccagc 1134
 ctggccaaaa attacaccag agagacagag tcctccccat tggAACAGG gtgattgagg 1194
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 gtaattttgc tcatttttat taaacttctg gtttacctga tgcttggctt cttttagggc 1374
 tacccttccatc tcattttctt tagccgtgt gcctgtaact ctgaggggg gcacccagtg 1434
 ggggtctgag tggcagaat ctcagaaggt ctcctgaac cgtccgcgcga ggcctgcagt 1494
 gggcctgcct ctccttgc tccctaacag gaaggtgtcc agttcaagag aacccaccca 1554
 gagactggga gtggggcgc acgcctataa tccctgcgtt ttggcagtcc gagggcagggg 1614
 aattgcttga actcaggagt tggagaccag cctggcaac atggcaaaac gcagtctgta 1674
 caaaaaatac aaaaaattag ccaggtgtag gggtaggcac ctggcatccc agctactcca 1734
 ggggctgagg tgacagcatt gcttaagccc agaaggtcga ggctgcagtg agctgagatc 1794
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 gggcgccgc 1864

<210> 11
 <211> 160
 <212> PRT
 <213> Homo sapiens

 <400> 11

103

Leu Phe Asp Ser Leu Ser Val Val Leu Ser Leu Ser Gly Ala Ser Pro
 1 5 10 15

Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val
 20 25 30

Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala
 35 40 45

Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu
 50 55 60

Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn
 65 70 75 80

Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe
 85 90 95

Arg Lys Gln Tyr Val Arg Arg Arg Trp Lys Leu Ser Phe Ser Ile Val
 100 105 110

Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu
 115 120 125

Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp
 130 135 140

Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Ser Ser Thr Ser
 145 150 155 160

<210> 12

<211> 480

<212> DNA

<213> Homo sapiens

<220>

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<222> (1)..(480)

<400> 12

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 Leu Phe Asp Ser Leu Ser Val Val Leu Ser Leu Ser Gly Ala Ser Pro
 1 5 10 15

ttc ctg gga gac acg aag cag gaa aca ctg gca aat atc aca gca gtg 96
 Phe Leu Gly Asp Thr Lys Gln Glu Thr Leu Ala Asn Ile Thr Ala Val
 20 25 30

agt tac gac ttt gat gag gaa ttc ttc agc cag acg agc gag ctg gcc 144
 Ser Tyr Asp Phe Asp Glu Glu Phe Phe Ser Gln Thr Ser Glu Leu Ala
 35 40 45

aag gac ttt att cgg aag ctt ctg gtt aaa gag acc cgg aaa cgg ctc 192
 Lys Asp Phe Ile Arg Lys Leu Leu Val Lys Glu Thr Arg Lys Arg Leu
 50 55 60

104

aca atc caa gag gct ctc aga cac ccc tgg atc acg ccg gtg gac aac	240
Thr Ile Gln Glu Ala Leu Arg His Pro Trp Ile Thr Pro Val Asp Asn	
65 70 75 80	
cag caa gcc atg gtg cgc agg gag tct gtg gtc aat ctg gag aac ttc	288
Gln Gln Ala Met Val Arg Arg Glu Ser Val Val Asn Leu Glu Asn Phe	
85 90 95	
agg aag cag tat gtc cgc agg cgg tgg aag ctt tcc ttc agc atc gtg	336
Arg Lys Gln Tyr Val Arg Arg Trp Lys Leu Ser Phe Ser Ile Val	
100 105 110	
tcc ctg tgc aac cac ctc acc cgc tcg ctg atg aag aag gtg cac ctg	384
Ser Leu Cys Asn His Leu Thr Arg Ser Leu Met Lys Lys Val His Leu	
115 120 125	
agg ccg gat gag gac ctg agg aac tgt gag agt gac act gag gag gac	432
Arg Pro Asp Glu Asp Leu Arg Asn Cys Glu Ser Asp Thr Glu Glu Asp	
130 135 140	
atc gcc agg agg aaa gcc ctc cac cca cgg agg agg agc agc acc tcc	480
Ile Ala Arg Arg Lys Ala Leu His Pro Arg Arg Ser Ser Thr Ser	
145 150 155 160	
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g acg gca tta gcc aaa gaa cta aga gaa ctc cgg att gaa gaa aca aac	49
Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn	
1 5 10 15	
cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca	97
Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser	
20 25 30	
gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat	145
Glu Ser Ser Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp	
35 40 45	
ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct	193
Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala	
50 55 60	
cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg	241
Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly	
65 70 75 80	
ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa	289
Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu	

85	90	95	
gga acc ttg atg att aga gag acg tct gga gag aag cga tct ggc Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly 100	105	110	337
cac agt gac agc aat ggc ttt gct ggc cac atc aac ctc cct gac ctg His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu 115	120	125	385
gtg cag cag agc cat tct cca gct gga acc ccg act gag gga ctg ggg Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly 130	135	140	433
cgc gtc tca acc cat tcc cag gag atg gac tct ggg act gaa tat ggc Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly 145	150	155	481
atg ggg agc agc acc aaa gcc tcc acc ccc ttt gtg gac ccc aga Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg 165	170	175	529
gta tac cag acg tct ccc act gat gaa gat gaa gag gat gag gaa tca Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Asp Glu Glu Ser 180	185	190	577
tca gcc gca gct ctg ttt act agc gaa ctt ctt agg caa gaa cag gcc Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala 195	200	205	625
aaa ctc aat gaa gca aga aag att tcg gtg gta aat gta aac cca acc Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr 210	215	220	673
aac att cgg cct cat agc gac aca cca gaa atc aga aaa tac aag aaa Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys 225	230	235	721
cga ttc aac tca gaa ata ctt tgt gca gct ctg tgg ggt gta aac ctt Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu 245	250	255	769
ctg gtg ggg act gaa aat ggc ctg atg ctt ttg gac cga agt ggg caa Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln 260	265	270	817
ggc aaa gtc tat aat ctg atc aac cgg agg cga ttt cag cag atg gat Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp 275	280	285	865
gtg cta gag gga ctg aat gtc ctt gtg aca att tca gga aag aag aat Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn 290	295	300	913
aag cta cga gtt tac tat ctt tca tgg tta aga aac aca aga ata cta cat Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His 305	310	315	961
			320

aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp 325 330 335	1009
ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys 340 345 350	1057
ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala 355 360 365	1105
cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu 370 375 380	1153
cag cac aag cct ctg cta gtt gat ctc acg gta gaa gaa ggt caa aga Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg 385 390 395 400	1201
tta aag gtt att ttt ggt tca cac act ggt ttc cat gta att gat gtt Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val 405 410 415	1249
gat tca gga aac tct tat gat atc tac ata cca tct cat att cag ggc Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly 420 425 430	1297
aat atc act cct cat gct att gtc atc ttg cct aaa Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys 435 440	1333

<210> 14
<211> 444
<212> PRT
<213> Homo sapiens

<400> 14 Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn 1 5 10 15
Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Ser Glu Glu Ser 20 25 30
Glu Ser Ser Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp 35 40 45
Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala 50 55 60
Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly 65 70 75 80
Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu 85 90 95

Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly
 100 105 110
 His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu
 115 120 125
 Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Thr Glu Gly Leu Gly
 130 135 140
 Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly
 145 150 155 160
 Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg
 165 170 175
 Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Glu Asp Glu Ser
 180 185 190
 Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala
 195 200 205
 Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr
 210 215 220
 Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys
 225 230 235 240
 Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu
 245 250 255
 Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln
 260 265 270
 Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp
 275 280 285
 Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn
 290 295 300
 Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His
 305 310 315 320
 Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp
 325 330 335
 Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys
 340 345 350
 Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala
 355 360 365
 Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu
 370 375 380
 Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg
 385 390 395 400

Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val
405 410 415

Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly
420 425 430

Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys
435 440

<210> 15

<211> 1332

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1332)

<400> 15

acg gca tta gcc aaa gaa cta aga gaa ctc cgg att gaa gaa aca aac 48
Thr Ala Leu Ala Lys Glu Leu Arg Glu Leu Arg Ile Glu Glu Thr Asn
1 5 10 15

cgc cca atg aag aag gtg act gat tac tcc tcc tcc agt gag gag tca 96
Arg Pro Met Lys Lys Val Thr Asp Tyr Ser Ser Ser Glu Glu Ser
20 25 30

gaa agt agc gag gaa gag gag gaa gat gga gag agc gag acc cat gat 144
Glu Ser Ser Glu Glu Glu Glu Asp Gly Glu Ser Glu Thr His Asp
35 40 45

ggg aca gtg gct gtc agc gac ata ccc aga ctg ata cca aca gga gct 192
Gly Thr Val Ala Val Ser Asp Ile Pro Arg Leu Ile Pro Thr Gly Ala
50 55 60

cca ggc agc aac gag cag tac aat gtg gga atg gtg ggg acg cat ggg 240
Pro Gly Ser Asn Glu Gln Tyr Asn Val Gly Met Val Gly Thr His Gly
65 70 75 80

ctg gag acc tct cat gcg gac agt ttc agc ggc agt att tca aga gaa 288
Leu Glu Thr Ser His Ala Asp Ser Phe Ser Gly Ser Ile Ser Arg Glu
85 90 95

gga acc ttg atg att aga gag acg tct gga gag aag aag cga tct ggc 336
Gly Thr Leu Met Ile Arg Glu Thr Ser Gly Glu Lys Lys Arg Ser Gly
100 105 110

cac agt gac agc aat ggc ttt gct ggc cac atc aac ctc cct gac ctg 384
His Ser Asp Ser Asn Gly Phe Ala Gly His Ile Asn Leu Pro Asp Leu
115 120 125

gtg cag cag agc cat tct cca gct gga acc ccg act gag gga ctg ggg 432
Val Gln Gln Ser His Ser Pro Ala Gly Thr Pro Glu Gly Leu Gly
130 135 140

cgc gtc tca acc cat tcc cag gag atg gac tct ggg act gaa tat ggc	480
Arg Val Ser Thr His Ser Gln Glu Met Asp Ser Gly Thr Glu Tyr Gly	
145 150 155 160	
atg ggg agc agc acc aaa gcc tcc ttc acc ccc ttt gtg gac ccc aga	528
Met Gly Ser Ser Thr Lys Ala Ser Phe Thr Pro Phe Val Asp Pro Arg	
165 170 175	
gta tac cag acg tct ccc act gat gaa gat gaa gag gat gag gaa tca	576
Val Tyr Gln Thr Ser Pro Thr Asp Glu Asp Glu Asp Glu Ser	
180 185 190	
tca gcc gca gct ctg ttt act agc gaa ctt ctt agg caa gaa cag gcc	624
Ser Ala Ala Ala Leu Phe Thr Ser Glu Leu Leu Arg Gln Glu Gln Ala	
195 200 205	
aaa ctc aat gaa gca aga aag att tcg gtg gta aat gta aac cca acc	672
Lys Leu Asn Glu Ala Arg Lys Ile Ser Val Val Asn Val Asn Pro Thr	
210 215 220	
aac att cgg cct cat agc gac aca cca gaa atc aga aaa tac aag aaa	720
Asn Ile Arg Pro His Ser Asp Thr Pro Glu Ile Arg Lys Tyr Lys Lys	
225 230 235 240	
cga ttc aac tca gaa ata ctt tgt gca gct ctg tgg ggt gta aac ctt	768
Arg Phe Asn Ser Glu Ile Leu Cys Ala Ala Leu Trp Gly Val Asn Leu	
245 250 255	
ctg gtg ggg act gaa aat ggc ctg atg ctt ttg gac cga agt ggg caa	816
Leu Val Gly Thr Glu Asn Gly Leu Met Leu Leu Asp Arg Ser Gly Gln	
260 265 270	
ggc aaa gtc tat aat ctg atc aac cgg agg cga ttt cag cag atg gat	864
Gly Lys Val Tyr Asn Leu Ile Asn Arg Arg Arg Phe Gln Gln Met Asp	
275 280 285	
gtg cta gag gga ctg aat gtc ctt gtg aca att tca gga aag aag aat	912
Val Leu Glu Gly Leu Asn Val Leu Val Thr Ile Ser Gly Lys Lys Asn	
290 295 300	
aag cta cga gtt tac tat ctt tca tgg tta aga aac aga ata cta cat	960
Lys Leu Arg Val Tyr Tyr Leu Ser Trp Leu Arg Asn Arg Ile Leu His	
305 310 315 320	
aat gac cca gaa gta gaa aag aaa caa ggc tgg atc act gtt ggg gac	1008
Asn Asp Pro Glu Val Glu Lys Lys Gln Gly Trp Ile Thr Val Gly Asp	
325 330 335	
ttg gaa ggc tgt ata cat tat aaa gtt gtt aaa tat gaa agg atc aaa	1056
Leu Glu Gly Cys Ile His Tyr Lys Val Val Lys Tyr Glu Arg Ile Lys	
340 345 350	
ttt ttg gtg att gcc tta aag aat gct gtg gaa ata tat gct tgg gct	1104
Phe Leu Val Ile Ala Leu Lys Asn Ala Val Glu Ile Tyr Ala Trp Ala	
355 360 365	
cct aaa ccg tat cat aaa ttc atg gca ttt aag tct ttt gca gat ctc	1152

110

Pro Lys Pro Tyr His Lys Phe Met Ala Phe Lys Ser Phe Ala Asp Leu
370 375 380

cag cac aag cct ctg cta gtt gat ctc acg gta gaa gaa ggt caa aga 1200
Gln His Lys Pro Leu Leu Val Asp Leu Thr Val Glu Glu Gly Gln Arg
385 390 395 400

tta aag gtt att ttt ggt tca cac act ggt ttc cat gta att gat gtt 1248
Leu Lys Val Ile Phe Gly Ser His Thr Gly Phe His Val Ile Asp Val
405 410 415

gat tca gga aac tct tat gat atc tac ata cca tct cat att cag ggc 1296
Asp Ser Gly Asn Ser Tyr Asp Ile Tyr Ile Pro Ser His Ile Gln Gly
420 425 430

aat atc act cct cat gct att gtc atc ttg cct aaa 1332
Asn Ile Thr Pro His Ala Ile Val Ile Leu Pro Lys
435 440